

Fri Feb 17 09:07:52 2006

us-09-493-480-7.olig_p2n.rnpbn

GenCore version 5.1.7
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OW protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 14:14:14 / Search time 503.769 Seconds
(without alignments)

3000.161 Million cell updates/sec

Title: US-09-493-480-7
Sequence: 1 MDAALCRLGGLLALPFGA.....GFCPPDPANQGMVHNR 712

Scoring table:

Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Pgapop 6.0, Pgapext 7.0
Delop 6.0, Delext 7.0

Searched: 7204252 segs, 1061369211 residues

1

Total number of hits satisfying chosen parameters: 14406945

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DB=Published_Application_NA_New -OPT=fastp -SUFFIX=olig_p2n.rnpbn
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-ALIGN=15 -MODE=LOCAL -OUTP=PCO -NOMEXT -HANSI218-500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs05p
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-PAR1 TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -PGAPOP=6 -PGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Published Applications_NA_New:

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13: /cgn2_6/p/cdata/1/pub/pna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	653	91.7	3768	12	US-11-202-516-3
2	653	91.7	4350	7	US-10-826-585-27
3	653	91.7	4350	7	US-10-826-585-38
4	653	91.7	4350	8	US-10-770-726-18

5	653	91.7	4330	12	US-11-113-202-8
6	653	91.7	4330	12	US-11-113-202-29
7	566	73.5	4543	12	US-11-125-405-1
8	72	10.1	14949	12	US-11-112-908-49
9	72	10.1	157224	12	US-11-112-908-51
10	72	10.1	157224	12	US-11-112-908-51
11	72	10.1	157224	12	US-11-112-908-48
12	67	9.4	4062	12	US-11-128-061-469
13	67	9.4	4062	12	US-11-128-061-469
14	52	7.3	4335	12	US-11-128-049-469
15	24	3.4	170189	12	US-11-011-3324-71
16	24	3.4	170189	12	US-11-112-908-50
17	10	1.4	2762	6	US-09-325-0624-60426
18	3	1.3	1972	12	US-11-235-527-669
19	3	1.3	1972	12	US-11-235-527-669
20	9	1.3	4060	12	US-11-126-527-2581
21	9	1.3	4164	12	US-11-000-688-825
22	9	1.3	4164	12	US-11-189-041-58
23	9	1.3	5484	7	US-10-912-971-11
24	9	1.3	5484	8	US-10-955-0544-86
25	9	1.3	5484	12	US-11-113-202-15
26	9	1.3	5616	7	US-10-826-585-19
27	9	1.3	5616	12	US-10-826-585-19
28	9	1.3	5616	12	US-11-113-202-5
29	9	1.3	156944	12	US-11-145-586-21
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31	8	1.1	25	12	US-11-121-849-20723
32	8	1.1	25	12	US-11-121-849-20724
33	8	1.1	25	12	US-11-121-849-20725
34	8	1.1	25	12	US-11-121-849-20726
35	8	1.1	25	12	US-11-121-849-20727
36	8	1.1	25	12	US-11-121-849-20728
37	8	1.1	25	12	US-11-121-849-20729
38	8	1.1	25	12	US-11-121-849-20730
39	8	1.1	25	12	US-11-121-849-20731
40	8	1.1	25	12	US-11-121-849-20732
41	8	1.1	25	12	US-11-121-849-20733
42	8	1.1	25	12	US-11-121-849-20734
43	8	1.1	25	12	US-11-121-849-20735
44	8	1.1	25	12	US-11-121-849-20736
45	8	1.1	25	12	US-11-121-849-20737

ALIGNMENTS

RESULT 1
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Sequence 3, Application US/11/202516
Publication No. US2006000465A1
GENERAL INFORMATION:
SEQUENCE: 3768
SEQUENCE: 4350
SEQUENCE: 4350
SEQUENCE: 4350
APPLICANT: Karlsson, Gunnilla
APPLICANT: Leach, Dana
APPLICANT: Nielsen, Klaus
APPLICANT: Rasmussen, Peter
TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
CURRENT APPLICATION NUMBER: US/11/202, 516
PRIORITY DATE: 2001-04-04
PRIORITY APPLICATION NUMBER: US 09/066, 703
PRIORITY FILING DATE: 2001-04-04
PRIORITY APPLICATION NUMBER: PCT/DK99/00525
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: DK 1998 01261
PRIORITY FILING DATE: 1998-10-05
PRIORITY APPLICATION NUMBER: US 60/105, 011
PRIORITY FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0

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Page 2

Best Local Similarity:	100.0%	Mismatches
Query Match:	91.7%	Indels:
DB:	6	Gaps:
US-09-493-480-7 (1-712)	x	US-10-207-498-5 (1-3765)

[illegible][illegible]

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US-09-493-480-7.01ig_p2n.rmpbm

Page 1

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 14:10:40 ; Search time 1147.23 Seconds

(without alignment)

Title: US-09-493-480-7

Sequence: 1 METALCRRGILLALIPGCA.....GFPCDPAPAGGWHRRR 712

Scoring table:

Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 413468905 residues

Words: 1

Total number of hits satisfying chosen parameters: 19572565

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:
-O4/abs/ASSIGN -pool/US09493480/runat 15022006 120212 28200/APP query.fasta.1
-DBpublished Applications NA main -OPMT-faster -START=1 -END=1 -MATRIX=0.150
-MINMATCH=0.1 -LOOPTC=0 -LOEXT=0 -INITTS=bits -START=1 -END=1 -MATRIX=0.150
-TRANS-human0.cdt -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=0
-ALIGN=15 -MODE=LOCAL -OUTPMT=PCO -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-YGAPOP=60 -YGAEXT=60 -DELOP=6 -DELEXT=7

Database: Published Applications NA main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	653	91.7	3768	3	US-09-811-113-8	Sequence 8, Appl1
3	653	91.7	3768	3	US-09-811-113-8	Sequence 2, Appl1
4	653	91.7	3768	3	US-09-853-362-6	Sequence 1, Appl1
5	653	91.7	3768	3	US-09-853-362-6	Sequence 1, Appl1
6	653	91.7	3768	3	US-09-930-115-1	Sequence 1, Appl1
7	653	91.7	3768	3	US-09-984-092-3	Sequence 3, Appl1

8	653	91.7	3768	6	US-10-313-644-1	Sequence 1, Appl1
9	653	91.7	3768	7	US-10-280-576-3	Sequence 3, Appl1
10	653	91.7	3768	7	US-10-441-779C-3	Sequence 3, Appl1
11	653	91.7	3768	7	US-10-384-339C-52	Sequence 52, Appl1
12	653	91.7	4473	3	US-09-441-411-5	Sequence 5, Appl1
13	653	91.7	4473	3	US-10-146-473-32	Sequence 32, Appl1
14	653	91.7	4473	5	US-10-207-655-44	Sequence 44, Appl1
15	653	91.7	4473	6	US-10-101-510-81	Sequence 81, Appl1
16	653	91.7	4473	8	US-10-762-128-5	Sequence 8, Appl1
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32	653	91.7	4473	8	US-10-762-128-5	Sequence 8, Appl1
33	653	91.7	4473	8	US-10-762-128-5	Sequence 8, Appl1
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41	653	91.7	4473	8	US-10-762-128-5	Sequence 8, Appl1
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43	653	91.7	4473	8	US-10-762-128-5	Sequence 8, Appl1
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ALIGNMENTS

RESULT 1
US-10-207-498-5
Sequence 5, Application US/10207498
Publication No. US2003014356A1
GENERAL INFORMATION:
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
FILE REFERENCE: 30448.103-US-01
CURRENT APPLICATION NUMBER: US/10/207-498
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 60/308,431
NUMBER OF SEQ ID NOS: 24
SOURCE: Passed for Windows Version 4.0
LENGTH: 3765
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3765)
US-10-207-498-5
Alignment Scores:
Score: 0
Percent Similarity: 100.0%

Fr1 Feb 17 09:07:52 2006

us-09-493-480-7.01ig_p2n.rni

Page: 2

TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
US-09-146-283-5

Alignment Scores:	
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Score:	651.00
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Best Local Similarity:	100.0%
Query Match:	91.7%
DB:	2
Length:	2385
Matches:	653
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-493-480-7 (1-712) X US-09-146-283-3 (1-2385)

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QY	261	SerGlyTLeuGlyLeuHisGCTProAlaLeuValaThrGlyAlaThrPheThrPheLeu	280
Dp	791	AGGAGCTACCTGAGAGATCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC	850
QY	281	SerMetProAspProGluGlyAspGlyThrPheGlyAlaSerCYSValaThrAlaCYSPro	300
Dp	851	TCCAGCGCCCAATCCCAAGGGCGCGGTACAATTCGCGGCGCAGCTGTGTGACGCTCTGCC	910
QY	301	TyrAlaGlyTLeuSerThrAspValaGlySerCYSThrLeuValaCYSProLeuHisGAlaGln	320
Dp	911	TACAACCTACCTTTTTCAGACAGGGAGATCTCCGACCGCTGTGTGCGCCCGCCCGCCCGCA	970
QY	321	GluValaThrAlaGluAspGlyThrThrIleAspGlyLeuGlySerGlySerProCYSAlaArg	340
Dp	971	GAGGTACAGCAGAGGATTCGAAACACACCGGTGTGTAAAGATTCAGACAGCCCTGTGCCCA	1030
QY	341	ValCYSerGlyLeuGluTMetGluHisGLeuThrGlyValaArgAlaValaThrSerAlaAsn	360
Dp	1031	GTCGTCTATAGGCTGTGGGCGAGAGACATCTTGCGAGAGGTGAAGGCAAGTTACAGCGCAAT	1090
QY	361	TLeuGlnIlePheAlaGlyCYSLeuValaGlyIlePheGlyIleSerLeuPheAspProIleSer	380
Dp	1091	ATCCAGATCTGT	1150
QY	381	PheAspProIleAspProAlaSerSerAlaThrAlaProLeuGlnProGluGlnGlnValaPhe	400
Dp	1151	TTTGTATGGGAGCCCAAGCTCTCAACATCGCCCGCTGTCAGGCGAGACAGCTCCAGAGTTT	1210
QY	401	GluThrIleGlnGlnGluThrGlyTLeuTyrIleSerAlaThrProAspSerLeuPro	420
Dp	1211	GAACTCTGTGAAGATCCAGGATCTTACTATCACTTCAGACAGTGAAGCCCAAGCCGCTCT	1270
QY	421	AspLeuSerAlaPheIleAlaGluGlnValaIleAspGlyValaGluIleAlaHisGlyAla	440
Dp	1271	GACCTCAGGCTCTTCCAGAACCTCGACAGTATCCCGGAGCAAAATTCCTGTCACATAGCGCC	1330
QY	441	TyrSerIleGlyThrLeuGluGlyLeuGlyIleSerTProLeuGlyLeuAspSerLeuGlu	460
Dp	1331	TACTGCGTGAACCTGTGAAGGGCTGGGATCGAGTGTGGAGGTGGAGTCTGACATCAAGAGAA	1390
QY	461	LeuGlySerGlyLeuAlaIleGlnIleAlaThrIleIleGlnIleValaGlnIleThrVala	480
Dp	1391	CTGGGACAGATCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1450
QY	481	ProThrPheGluIleuPheAspArgProIleGlnIleGluHisGlyThrAlaAlaHisGPro	500
Dp	1451	CCCTGGGACAGGCTCTTTCGGAAAGCCCGACACAGACTGTGTCTGACATCTGCAACCGGCGCA	1510
QY	501	GluAspProIleCYSValaGlyGlnGlyLeuAlaCYSHisGlnLeuGlyAlaIleArgIleCYS	520
Dp	1511	GAAACACAGGT	1570
QY	521	ThrGlyProGlyIleProGlnGlyValaAspCYSerGlyIlePheLeuAlaArgIleGlnGluCYS	540
Dp	1571	TGGGGTCCAGAGGCCCAACGATGTGTACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1630
QY	541	ValGlnGluCYSValaGlyIleuGlnGlyLeuProArgGlnGlyTyrAlaAlaHisGlyCYS	560
Dp	1631	GTCGAGGAGATTCGACATCTGTGCAAGGGGCTGCCCGAGAGATTAAGATTCGACGACAGCT	1690
QY	561	LeuProCYSHisIleProGluCYSLeuIleProGlnAlaHisGlyIleSerValaThrCYSArgIlePro	580
Dp	1691	TTCGCGTCAAGGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCT	1750
QY	581	AlaAspProIleCYSValaHisGlyTyrLeuAspArgProIleProHisCYSValaIleAspGly	600
Dp	1751	GCTGACACAGGT	1810
QY	601	ProSerGlyValaIleProAspLeuSerTyrMetProIleTrrIleProIleProAspGluGln	620

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 14:09:37 ; Search time 230.3 seconds
(without alignments)
4359.704 Million cell updates/sec

Title: US-09-493-480-7

Perfect score: 712
Sequence: 1 MELALCRWGLLALPPGA.....GFCPCDPAPAGAGWYHRR 712

Scoring table: OM-60

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Pgapop 6.0 , Pgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Wc: 1

Total number of hits satisfying chosen parameters: 2539977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-TRANS=mm40 -M40=1 -M40=1 -M40=1 -M40=1 -M40=1 -M40=1 -M40=1 -M40=1 -M40=1 -M40=1
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-MAXLEN=2000000000 -HOST=absae03p
-USER=US09493480 -GCN 1.1 359 -runat.15022006.120209.28128 -NCPU=6 -ICPU=3
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-PARV TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -PAPOP=6 -PAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	653	91.7	2385	2	US-09-146-283-3
2	653	91.7	2385	2	US-08-579-823A-3
3	653	91.7	2385	2	US-09-344-195-3
4	653	91.7	3768	2	US-08-625-101-1
5	653	91.7	3768	2	US-08-356-786-1
6	653	91.7	3768	2	US-08-811-115-2
7	653	91.7	3768	2	US-08-811-115-2
8	653	91.7	4473	2	US-09-046-804-1

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ALLEGMENTS

RESULT 1
US-09-146-283-3
Sequence 3, Application US/09146283.
Patent No. 5976546
GENERAL INFORMATION:
APPLICANT: Laus, Retner
INVENTOR: Laus, Retner
ATTORNEY: Ruesig, Curtis L.
NUMBER OF INVENTORS: 1
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: COMPOS/JE-POS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09146,283
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R. 42,702
REGISTRATION NUMBER: 7636-0010.21
REFERENCE/DOCKET NUMBER:
TELEPHONE: 650-324-0880

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US-09-493-480-7 (1-712) x DQ047380 (1-3695)

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QY 66 ProThAmAlaserleuSerPheleuGlnAplleGlnGlnvalGlnGlnYTYValleu 85
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QY 106 GlnleuPheGlnapmetYalaleuvalaleuapnglYasProleuapmet 125
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QY 166 ThrlleuYrclngYcygslnglvalnglYasleuclYleuThyleu 185
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QY 246 GlnYleuYrclngYcygslnglvalnglYasleuclYleuThyleu 265
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QY 266 LeuHlaserleuYrclngYcygslnglvalnglYasleuclYleuThyleu 285
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DQ04218
LOCUS
DEFINITION
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  1 (bases 1 to 762)
  Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
  Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, H.,
  Zhang, X., Zeng, G., and He, G. full-length human cDNAs directly from
  human libraries optimized for large and rare transcripts
  Unpublished (2005)
  CONTACT: Kovacs, K
  High Throughput cDNA Cloning
  Origene Technologies, Inc. (www.origene.com)
  6 Telf Court, Suite 100, Rockville, MD 20850, USA
  Tel: 301 340 3188
  Fax: 301 340 8606
  Email: cDNA@origene.com
  This EST submission is part of an on-going human full-length
  cloning project at Origene Technologies, Inc.
  Please contact Origene for access.
  Origene Technologies, Inc.
  6 Telf Ct Suite 100
  Rockville, MD 20850
  Tel: (301) 340-3188
  http://www.origene.com
  Seq primer: PCMV5 Splice forward vector primer, Origene
  Technologies Inc.
  Location/Qualifiers
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      large inserts into mammalian expression vectors. Random
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      5' and 3' ends. cDNAs constructed and available from Origene
      Technologies"

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Fri Feb 17 09:07:53 2006

us-09-493-480-7.0119_p2n.rst

Page 1

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 14:05:40 / Search time 5780.69 seconds
(without alignments)
5762.704 Million cell updates/sec

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Sequence: 1

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Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

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Total number of hits satisfying chosen parameters: 82154962

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Using filter 45 summaries

Command line parameters:
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-OUT3=3 -STRK=1 -STRK2=1 -STRK3=1 -STRK4=1 -STRK5=1 -STRK6=1 -STRK7=1 -STRK8=1 -STRK9=1 -STRK10=1
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8: gb.est8.*
9: gb.gseq1.*
10: gb.gseq2.*
11: gb.gseq3.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Query No.	Score	Match Length	DB ID	Description
1	324	45.5	3695 11	DD047380
2	228	32.2	762 8	DR004218
3	228	32.0	1016 3	BM562913
4	218	30.6	894 2	BE746725
5	207	29.1	523 7	CV743369
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7	203	28.5	2004 4	CR592336

8	200	28.1	817 8	CV754715
9	196	27.7	618 7	CV571007
10	185	27.4	605 7	CM409745
11	184	27.2	583 3	BP315895
12	183	27.1	582 3	BP313449
13	182	27.0	576 3	BP332775
14	188	26.4	566 7	CM409736
15	185	26.0	622 7	CM409753
16	182	25.6	589 7	CM409734
17	181	25.4	659 7	CM409714
18	179	25.1	614 1	AM370693
19	175	23.2	581 3	BP333868
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23	156	21.9	582 3	BP315146
24	148	20.8	561 3	BM720098
25	144	20.2	581 3	BP314186
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36	124	17.4	1009 5	BM472419
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DEFINITION	Homo sapiens ERBB2 gene, VIRUTAL TRANSCRIPT, partial sequence.				
ACCESSION	DD047380				
VERSION	DD047380.1	GI:66900579			
KEYWORDS	GENE				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 3695)				
AUTHORS	Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Shiner, J.J., Adams, M.D. and Cargill, M.				
TITLE	A scan for positively selected genes in the genomes of humans and chimpanzees				
REFERENCE	PLoS Biol. 3 (6), E170 (2005)				
REFERENCE	2 (bases 1 to 3695)				
AUTHORS	Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Shiner, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Substitution				
REFERENCE	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
REFERENCE	15669125				
COMMENT	This sequence was made by sequencing genomic exons and ordering them on alignment. Translation starts at the beginning of alignment.				

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361 T[ac]ngl"phea]ag]wCvnlsvl"vrl"epheg]vSerLeuAlaPheLeuProG]User 380

[illegible]

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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	91.7%	Indels:	0
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US-09-493-480-7 (1-712) X CS020247 (1-2028)

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US-11-202-516-3

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DB:             12
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Length:      3768
Matches:     653
Conservative: 0
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US-09-493-480-6 (1-919) X US-11-202-516-3 (1-3768)

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Dh	841	TCGATGCCCATCCCGAGCGCGGATGATGACATGTGGCGTCTGAGTGTGACGCTGCTGCC	900
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Dh	901	TAACACACTCTTCTTGGAGATCTGGAGATCTGCGACCTCGTCTCCCTCCCTCAACCAA	960
Oy	321	GluValThiAlaGlyValSerGlyThiGlnTyrGlyValGlySerGlyProGlyAlaTyr	340
Dh	961	GAGGTGACAGACAGAGATGAGACACAGCGCGGTGTGAGAAAGTGCACAAAGCTGTGCCCA	1020
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Dh	1021	GTCGTCATGATGTCTGGCGAGAGACATCTGGACAGAGATCGAGAGCGATTTACAGTCCGANT	1080
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Dh	1081	ATCCAGGAGATTTGCGTGTGTCCAAAGATCTTTGGAGACCTGGCAATTTCTCCGAGAGCG	1140
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Oy	421	AlaLeuSerValPheThiAlaAlaGlnValThiAlaGlyTyrThiLeuThiGlnAlaGlyAla	440
Dh	1261	GACCTCAGCGCTTCCAAACACTCGAGATGATATCCGGGAGAGAAATTCGACATAGCGGCC	1320
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Oy	481	ProTyrAlaGlnLeuPheAlaGlyAlaProThiGlnAlaLeuLeuThiIleThiAlaAlaAlaPro	500
Dh	1441	CCCTGGGACGACGCTCTTTGAGAACCCGACACGACGCTGCTCAACATCTGACACGACCA	1500
Oy	501	GluAlaProGlyValAlaGlyLeuGlyLeuAlaCysGlyIleGlyValAlaGlyAlaGlySer	520
Dh	1501	GAGACACAGTGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1560
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Dh	1561	TGGGGATCGAGGGCCACACAGATGTGTCACTGACGACGATGTTCTTCCGGGCGAGAGATG	1620
Oy	541	ValGlnGlyCysAlaGlyValLeuGlnGlyLeuProAlaGlyTyrValaAlaAlaGlySer	560
Dh	1621	GTTGAGGAGATGTCGACATGACGAGGAGCTCTCCCGAGAGATGTATGTATATCCAGACGCT	1680
Oy	561	LeuProGlnPheAlaProGlyLeuGlyProGlnAlaGlyValThiCysPheGlyTyrProGly	580
Dh	1681	TTTCCGTGTCCACCTGATGTGACGCCCCGAGAAATGTGTCAAGATCCTTTTGTGACCGGAG	1740
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Dh	1741	GCTGACACAGGTGTGACCTGTGTGCTGATTAAGAGACCTCCCTCTGTGCTGACGCTGCTG	1800
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Fri Feb 17 09:07:51 2006

US-09-493-480-6.015_p2n.rmpbm

Page 1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OK protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 14:10:40 / Search time 1480.77 Seconds
(without alignment)

5132.175 Million cell updates/sec

Title: US-09-493-480-6

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Ygapop 60.0, Ygapext 60.0
Egapop 6.0, Egapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 413468905 residues

Model size: 1

Total number of hits satisfying chosen parameters: 19572565

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Prod No is the number of results predicted by chance to have a
score greater than the highest score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
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2	653	71.1	3768	3	US-09-811-123-8
3	653	71.1	3768	3	US-09-811-123-8
4	653	71.1	3768	3	US-09-811-123-8
5	653	71.1	3768	3	US-09-811-123-8
6	653	71.1	3768	3	US-09-811-123-8
7	653	71.1	3768	3	US-09-811-123-8

8	653	71.1	3768	6	US-10-313-644-1	Sequence 1, Appl1
9	653	71.1	3768	7	US-10-280-576-3	Sequence 3, Appl1
10	653	71.1	3768	7	US-10-441-779C-3	Sequence 3, Appl1
11	653	71.1	3768	7	US-10-384-339C-52	Sequence 52, Appl1
12	653	71.1	4473	3	US-09-441-411-5	Sequence 5, Appl1
13	653	71.1	4473	5	US-10-146-473-32	Sequence 32, Appl1
14	653	71.1	4473	5	US-10-207-655-44	Sequence 44, Appl1
15	653	71.1	4473	5	US-10-101-510-81	Sequence 81, Appl1
16	653	71.1	4473	8	US-10-762-128-5	Sequence 5, Appl1
17	653	71.1	4473	8	US-10-723-860-8	Sequence 8, Appl1
18	653	71.1	4473	3	US-09-811-123-8	Sequence 11, Appl1
19	653	71.1	4473	3	US-09-811-123-8	Sequence 11, Appl1
20	653	71.1	4473	3	US-10-007-926A-119	Sequence 119, Appl1
21	653	71.1	4473	6	US-10-338-730-1	Sequence 1, Appl1
22	653	71.1	4473	6	US-10-116-275-131	Sequence 124, Appl1
23	653	71.1	4473	6	US-10-116-275-131	Sequence 11, Appl1
24	653	71.1	4473	6	US-10-426-836-11	Sequence 11, Appl1
25	653	71.1	4473	6	US-10-212-437A-27	Sequence 27, Appl1
26	653	71.1	4473	6	US-10-117-937-595	Sequence 595, Appl1
27	653	71.1	4473	6	US-10-392-113-45	Sequence 45, Appl1
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31	653	71.1	4473	7	US-10-435-696-10	Sequence 30, Appl1
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33	653	71.1	4473	9	US-10-928-465-75	Sequence 75, Appl1
34	653	71.1	4473	9	US-10-794-514A-2	Sequence 2, Appl1
35	653	71.1	4473	9	US-10-871-708-18	Sequence 18, Appl1
36	653	71.1	4473	10	US-11-067-064-595	Sequence 595, Appl1
37	653	71.1	4473	10	US-11-067-199-595	Sequence 595, Appl1
38	653	71.1	4473	3	US-09-971-392-70	Sequence 70, Appl1
39	653	71.1	4473	3	US-10-198-846-10896	Sequence 10896, Appl1
40	653	71.1	4473	3	US-09-811-123-8	Sequence 7, Appl1
41	653	71.1	4473	3	US-09-811-123-8	Sequence 7, Appl1
42	653	71.1	4473	3	US-10-956-373-1	Sequence 1, Appl1
43	653	71.1	4473	6	US-10-412-804A-3	Sequence 3, Appl1
44	653	71.1	4473	6	US-10-412-804A-3	Sequence 3, Appl1
45	653	71.1	4473	5	US-09-765-506-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-10-207-498-5
Sequence 5, Application US/10207498
Publication No. US2003014356A1
GENRUL INFORMATION:
APPLICANT: Elizabeth Singer
APPLICANT: David E. Sliemers
APPLICANT: David E. Sliemers
TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
FILE REFERENCE: 30448.103-US-01
CURRENT FILING DATE: 2002-07-29
PRIORITY FILING DATE: 2001-07-27
PRIORITY SEQ ID NOS: 24
PRIORITY SEQ ID NOS: 24
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 3765
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3765)
US-10-207-498-5
Alignment Scores:
Percent Similarity: 100.04
Length: 3765
Matches: 653
Conservative: 0

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us-09-493-480-6.01ig_p2n.rn1

Page 2

TELEFAX: 650-344-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2363 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HSR-2 fusion gene; Fig. 8
US-09-146-283-3

Alignment Scores:
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Score: 653.00 Matches: 653
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 71.1% Indels: 0
Gaps: 2 0

US-09-493-480-6 (1-919) x US-09-146-283-3 (1-2385)

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QY 21 AAlaSerThrGlnValCyethrGlnYThAARMeLeuAlaLeuProAlaSerProGlu 40
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QY 101 IleValAlaGlnYThrGlnLeuPheGlnAlaAlaSerYAlaLeuAlaValAlaAlaAlaGln 120
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DB 851 TCGATCCGACATCCCGAGGAGCGAGTACCTGGAGCGAGTGGAGTGGAGTGGAGTGGAG 910
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QY 501 GlnAlaGlnYCyValAlaGlnYAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 520
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DB 541 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1600
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DB 1721 GCTGACGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1810
QY 601 ProSerGlyValYProAlaAlaSerYThPheProLeuYThPheProAlaAlaGlnY 620

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US-09-493-480-6.01lg_p2n.rn1

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 14:09:37 ; Search time 374.7 Seconds
(without alignments)
4359.704 Million cell updates/sec

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Select score: 919

Scoring table: Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2599977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: filtering filter 45 summaries

Command line parameters:
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-DOFCU=0 -DOPEXT=0 -OUTR=abite STR=1 -END=1 -PAR=ol1lg_p2n.rn1
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-USER=US09493480 QCEN 1.1 359 epurat.15022006.120209.28128 -NCPU=6 -ICPU=3
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-VARI TIMEOUT=30 -THREDS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6 -Fgapext=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	653	71.1	3768	2	US-09-811-115-2
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11	653	71.1	4473	3	US-09-441-111.5
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13	653	71.1	4530	2	US-08-645-865-9
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15	653	71.1	4530	3	US-09-591-187A-1
16	653	71.1	4530	3	US-09-877-177A-11
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ALIGNMENTS

RESULT 1
US-09-146-283-3
Sequence 3, Appl 1
Patent No. 5976546
GENERAL INFORMATION:
APPLICANT: Laus, Retner
APPLICANT: Ruegg, Curtis L.
TITLE OF INVENTION: Immunostimulatory Compositions
INVENTOR: Laus, Retner
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: IBM PC compatible
CURRENT APPLICATION DATA:
Application Number: US/09/146,283
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880

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ORIGIN

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 Query Match: 320.3% Indels: 0
 DB: 11 Gaps: 0

US-09-493-480-6 (1-919) x DQ047380 (1-3695)

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 DB 123 CCACCAATCCAGGCT 182
 OY 86 HisAlaHisAlaSerProAlaSerProGluThrHisLeuApMeL 105
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 OY 106 HisLeuAlaSerProAlaSerProGluThrHisLeuApMeL 125
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 DB 783 GAGGCTCGGTATCATTTGGGCGCAGCTGTGACCTGCTCTCTCTCTCTCTCTCTCTCT 842
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 OY 346 GTCATGATGCT 349
 DB 963 GCGATGAGCAC 974

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 VERSION
 EST_24905427
 KEYWORDS
 EST
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 ORGANISM
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE
 1 (bases 1 to 885)
 NIH-MGC http://mgc.ncl.nih.gov/
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 CONTACT
 Robert Strausberg, Ph.D.
 Email: csapsb-remail.nih.gov
 Tissue Procurement: Kristi A. Eglund, Iva Pastan
 cDNA Library Prepared by: The I.M.A.G.E. Consortium (LMU)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMU, at:
 http://image.llnl.gov
 Plate: LHM14285 row: 1 column: 17
 High quality sequence stop: 717.

FEATURES
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 HBLT-HMEL, LNCaP"
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 /clone_id="MAFOL"
 /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
 Subtracted with brain, liver, lung, kidney and muscle.
 Directionally cloned. Priming method: oligo-dT. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James V. Vincent, Robert Strausberg,
 Bunkook Lee & Iva Pastan: Directly derived cDNA library
 from primary mammary gland medullary and secreted proteins.
 Manuscript submitted."

ORIGIN

Alignment Scores:
 Pred. No.: 8.18e-251 Length: 885
 Score: 261.00 Matches: 261
 Percent Similarity: 100.0% Conservative: 0
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 Query Match: 28.4% Indels: 0
 DB: 6 Gaps: 0

US-09-493-480-6 (1-919) x CA455074 (1-885)

Fr1 Feb 17 09:07:51 2006

us-09-493-480-6.011g_p2n.png

Page 2

PA (RICE) 1ST RICERCHIE BIOL. MOLECOLARE ANGELETTI.
XX
XX Gallo P., Monaci P., Nuzzo M;
PI
PI WPI.; 2005-123289/13.
DR WPI.; 2005-123289/13.
DR P-PSDB; ADW87401.
XX
XX New synthetic nucleic acid molecule encoding human epidermal growth factor 2 (HER2)/neu or HER2/CDTM protein, useful for preventing or treating HER2-associated cancer.
PT
PT
PS Claim 7; SEQ ID NO 9; 62pp; English.
XX
XX The invention relates to a synthetic nucleic acid molecule which CC
CC comprises a sequence of nucleotides: (a) encoding a human epidermal CC
CC growth factor 2 (HER2)/neu protein; (b) encoding a human HER2/CDTM CC
CC protein; and (c) encoding a vaccine "composition" composition, and methods CC
CC useful for preventing or treating HER2-associated cancer. The present CC
CC sequence represents the human codon-optimized HER2/CDTM DNA.
XX
XX Sequence 2028 BP; 338 A; 802 C; 619 G; 269 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	0
Score:	653.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	71.1%
DB:	
	length: 2028
	Matches: 653
	Conservative: 0
	Mismatch: 0
	Indels: 0
	Gaps: 0

US-09-493-480-6 (1-919) X ADW87396 (1-2028)

[illegible]

OY	202	GLYSRSTCYSTRDGLVGRSESGEGLVMSRSGEGLSETHRYTHRYVAL	220
DB	601	GGACCCGCTCTGGGGGCGAGGACGAGGAGACTCGACAGAGCTGACCCGACCCCTGGC	660
OY	221	ALAAGLYCYVALAATCYVALSEGLYPROLEUPROTHIRAPGYSGLYSGLIAGLIAGLI	240
DB	661	GGGCGACGCTGGGCGCCGCTGGGCGGACGCTGACCACTGACCACTGACCACTGACGTC	720
OY	241	ALAALATCYSTRDGLYPRODYHHSISSETRAPGYSGLIAGLYGLYSGLIAPHEANHS	260
DB	721	GGCGCGGGCTGACCGGGCCGAGGAGACGACCTGGCGCTGGCTGACCTGACCTGACCAAC	780
OY	261	SEGLIYLCYSGVLSLEHISSECYPROALALEUVALTHRYTASHTHAPRTHPHEGLU	280
DB	781	AGGGCATCTCGAGAGCTGACCTGGCGCGCGCTGGAGACTGACACGACCACTGACCTGAC	840
OY	281	SEHTPEPROAMPRODGLIYATGTYTHPHEGLIYSECYVALTHRYTASCPAPRO	300
DB	841	AGCGACCGCGACCGCGACCGCGCGCTGACCTGGCGCGAGCTGAGCGACCGCGCGCGCC	900
OY	301	TYRANTHYLEUSETRTHAPRVALGYSECYSTRHLEUVALCYSPROLEHISLAPMANGL	320
DB	901	THACATCTCTGACGACCGACGAGGAGGACGCTGACCCCTGGTGGCGCCCTGCAACCAAC	960
OY	321	GLIVALTHRYALGLVMSRGLYTHRYTHRYAGCYSEGLYSECYVALATG	340
DB	961	GAGTGTGACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1020
OY	1021	GTGTGTGACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1080
OY	361	ILSGNLIPHEALADLYCYALYSEGLYLEPHGLYSEGLYSLEUVALAPHELEUPROGLUSE	380
DB	1081	ATCGAGAGGCTGGCGCGCTGCAAGAACTTCTGGAGACTCTGCTCTGCGCGAGAGC	1140
OY	381	PHEASPGIYASPPROALASERANTHRYALAPROLEUGLNPFGGLIYLENGLYLAPHE	400
DB	1141	TTGACAGGAGGACCGCGACGACGACCGCGCGCGCTGACGCGACGACGAGCGAGCTTC	1200
OY	401	GLIYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTH	420
DB	1201	GAGACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	440
OY	421	ASPLEUSEYTAIPHEGLYAPHEGLYVALIYLENGLYYAGGLILEUVALAPHEGLYVAL	440
DB	1261	GACCTTGAGGCTGCTGACAGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1320
OY	441	TYRSTLETHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTH	460
DB	1321	THACATCTGACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1380
OY	461	LEUGLYSEGLYLEUVALALEUVALHSISSETRAPGYSGLIAGLYGLYSGLIAPHEANHS	480
DB	1381	CTGGGACGAGGCTGGCGCTGGAGTACGACCAACGACCGCTGGCTGGCTGACCTGACCTG	1440
OY	481	PROCTPRAPRODGLIYATGTYTHPHEGLIYSECYVALTHRYTASHTHAPRTHPHEGLU	500
DB	1441	CGCTTGAGGACCGCGACCGCGACCGCGACCGCGACCGCGACCGCGACCGCGACCGCG	1500
OY	501	GLIAPRODGLYVALIYGLIYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY	520
DB	1501	GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1560
OY	521	TRPGIYPRODGLYPROTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTHRYTH	540
DB	1561	TGGAGGCTGGGCGCGACCGCGACCGCGACCGCGACCGCGACCGCGACCGCGACCGCG	1620
OY	541	VALIYGLIYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY	560
DB	1621	GTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1680
OY	561	LEUPROCYHISAPRODGLYGLIAGINTROGLIAPMANGLYSEVALTHRYTHRYTHRYTH	580

Fri Feb 17 09:07:51 2006

us-09-493-480-6.01ig_p2n.rge

GenCase version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 14:00:33 / Search time 11870.4 Seconds
(without alignments)
400,801 Million cell updates/sec

Title: US-09-493-480-6

Perfect score: 319
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Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 588141 seqs, 2842172563 residues

1

Total number of hits satisfying chosen parameters: 11757827

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Database:

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Prod. No. is the number of results predicted by change to have a score greater than or equal to the product of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	653	71.1	2385	6	AR098963	AR098963 Sequence
5	653	71.1	3768	6	AR034479	AR034479 Sequence
6	653	71.1	3768	6	BD224136	BD224136 Novel met
7	653	71.1	3768	6	BD267514	BD267514 HER-2/neu
8	653	71.1	3768	6	CQ815384	CQ815384 Sequence
9	653	71.1	3768	6	CS007994	CS007994 Sequence
10	653	71.1	3768	6	CS020239	CS020239 Sequence
11	653	71.1	3768	6	CS104222	CS104222 Sequence
12	653	71.1	3768	6	AR409603	AR409603 Sequence
13	653	71.1	3768	6	AX060704	AX060704 Sequence
14	653	71.1	3768	6	AX204812	AX204812 Sequence
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19	653	71.1	3768	6	AY888050	AY888050 Synthetic
20	653	71.1	3768	6	AY888051	AY888051 Synthetic
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ALIGNMENTS

RESULT 1
LOCUS CS020247 2028 bp DNA linear PAT 23-FEB-2005
DEFINITION Sequence 9 from Patent WO2005012527.
ACCESSION CS020247.1 GI:60220905
VERSION CS020247.1
KEYWORDS
SOURCE
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 Gallo P.I., Monaci P.I. and Nuzzo M.I.
Synthetic gene encoding human epidermal growth factor 2/neu antigen
and uses thereof
JOURNAL Patent: WO 2005012527-A 9 10-FEB-2005
FEDERAL Institute of Research in Biologia Molecolare P. Angeletti S.P.A.
(It)

FEATURES

source
1..2028
Location/Qualifiers
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/note="HER2ECTMopt"

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Prod. No.: